STIC-Biotech/ChemLib

From: Sent:

Schultz, James

Monday, March 03, 2003 11:07 AM STIC-Biotech/ChemLib

Subject:

sequence search request for 10/003,919

Hello,

I need a length limited nucleotide sequence search performed on SEQ ID NO:3 (5273 nt long) in the above entitled case, where the maximum size of the returned hit is no longer than 50 nucleotides. Thank you very much, Doug Schultz

J. Douglas Schultz, Ph.D. AU 1635 (Biotechnology) Patent Examiner United States Patent and Trademark Office (703) 308-9355 (703) 746-3973 (fax) Office: CM1 12E18 Mail: CM1 11E12

> Point of Contact: Barb O'Bryen **Technical Information Specialist** STIC CM1 6A05 308-4291

Searcher: 18013
Phone:
Location:
Date Picked Up:
Date Completed: 3 12.03
Searcher Prep/Review:
Clerical:
Online time:

TYPE OF SEARCH:
NA Sequences:
AA Sequences:
Structures:
Bibliographic:
Litigation:
Full text:
Patent Family:
Other:

ENDOR/COST (where applic.)
STN:
DIALOG:
Questel/Orbit:
DRLink:
Lexis/Nexis:
Sequence Sys.:
WWW/Internet:
Other (specify):

BioTech-Chem Library Search Results Feedback Form (Optional)



The search results generated for your recent request are attached. If you have any questions or comments (compliments or complaints) about the scope or the results of the search, please contact the Bio Tech-Chem searcher who conducted the search or contact:

Mary Hale, Supervisor, 308-4258 CM-1 Room 1E01

Voluntary Results Feedback Form	
> I am an examiner in Workgroup: (Example: 1610)	
> Relevant prior art found, search results used as follows:	•
102 rejection	
103 rejection	´ .
Cited as being of interest.	
Helped examiner better understand the invention.	
Helped examiner better understand the state of the art in their technology.	
Types of relevant prior art found:	
Foreign Patent(s)	
Non-Patent Literature (journal articles, conference proceedings, new product announcements etc.)	
> Relevant prior art not found:	
Results verified the lack of relevant prior art (helped determine patentability	y).
Search results were not useful in determining patentability or understanding	g the invention.
Other Comments:	

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Title:
Perfect score:
Sequence:
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Patent: US 5582979-A 385 10-DEC-1996;

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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35; Conservation
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Sha,N., Walinton,J. and Patel,N.
Gene composition and method
Patent: JP 2000245487-A 601 12-SEP-2000;
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N Gene composition and method.

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JP 2002045487-A/602.

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27-JAN-1999 US 09/238.402
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AS Sha, N., Walinton, J. and Patel, N.

Gene composition and method

JOURNAL Patent; JP 2000245487-A 603 12-SEP-2000,
AFTMETRICS INC

COMMENT OS Unknown
PN JP 2000245487-A/603
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Gene composition and method
Paten: JP 2000245487-A 604 12-SEP-2000;
PATHETRICS INC

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OS UNKNOWN
PN JP 2000245487-A/604
PD 12-SEP-2000
PF 27-JAN-2000 JP 2000019392
PF 27-JAN-2000 JP 200019392
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Gene composition and method.

BD002938

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BD002939
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KEYWORDS
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BD00294
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                                                         27-JAN-2000 JP 2000019392
27-JAN-1999 US 09/238.402
NIRA SHA, JANET WALLINTON, NIRA
C12N15/09, C12Q1/68, C12N15/00
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cus	BD002939 31 bp DNA	linear	PAT 31-JAN-2002
EFINITION	Gene composition and method.		
CESSION	BD002939		
ERSION	BD002939.1 GI:18630900		
EYWORDS	JP 2000245487-A/605.		
DURCE	unidentified.		
ORGANISM	unidentified		
	unclassified.		
EFERENCE	1 (bases 1 to 31)		
AUTHORS	Sha, N., Walinton, J. and Patel, N.		
TITLE	Gene composition and method		
JOURNAL	Patent: JP 2000245487-A 605 12-SEP-2000;		
	AFIMETRICS INC		
DMMENT	OS Unknown		
	PN JP 2000245487-A/605		
	PD 12-SEP-2000		
	PF 27-JAN-2000 JP 2000019392		
	PR 27-JAN-1999 US 09/238.402		

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/db_xref="taxon:32644"	/organism="unidentified"	131	Location/Qualifiers	/organism='Unknown'.	source 131	Key Location/Qualifiers		C12N15/09, C12Q1/68, C12N15/00	٤	S	27-JAN-2000 JP 2000019392	12-SEP-2000	JP 2000245487-A/605	Unknown	AFIMETRICS INC	Patent: JP 2000245487-A 605 12-SEP-2000;	Gene composition and method	Sha, N., Walinton, J. and Patel, N.

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Socie 30.0; De control	arlty 96.88; pred. No. 1.18+05; pred. No. 1.18+05; preservative 1; Mismatches 0; pred. AGCCTCAGTGAGCTGCCAC 4099	ocal Similarity 96.8%; Pred. No. 1.1e-05; ocal Similarity 96.8%; Pred. No. 1.1e-05; s 30; Conservative 1; Mismatches 0; Indels 9 CCATGCAGTGAAGCCCTCAGTGAGCTGCCAC 4099
3%; Score 10.0; DB 3%; Pred. No. 1.1e+0 1; Mismatches TGAGCTGCCAC 4099	3%; Score 30.0; UB 0; 3%; Pred. No. 1.1e+05; 1; Mismatches 0; TGAGCTGCCAC 4099	** score 30.0; LB 0; Length 31; ** pred. No. 1.1e+05; 1; Mismatches 0; Indels **TGAGCTGCCAC 4099
30.6; DB NO. 1.1e+0 matches C 4099	matches 0; C 4099	30.5; UB 6; Length 31; No. 1.1e+05; matches 0; Indels C 4099
	0,	0; Length 31;

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	BD002940 31 bp DNA	linear	PAT	31.	JAN-	PAT 31-JAN-2002
NOLL	Gene composition and method.					
NOIS	BD002940					
ž	BD002940.1 GI:18630901					
ĝ	JP 2000245487-A/606.					
.,	unidentified.					
WSIN	unidentified					
	unclassified.					
NCE	1 (bases 1 to 31)					
ORS	Sha, N., Walinton, J. and Patel, N.					
য়ৈ	Gene composition and method					
NAL	Patent: JP 2000245487-A 606 12-SEP-2000;					
	AFIMETRICS INC					
a	OS Unknown					
	PN JP 2000245487-A/606					
	PD 12-SEP-2000					

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BD002942
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Sha, N., walinton, J. and Patel, N.
Gene composition and method
Patent: JP 2000245487-A 608 12-SEP-2000;
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Location/Qualifiers
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/db_xref="taxon:32644"
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9 c 9 g
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1.1e+05;
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Matches 30; Conserv
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OS UNKOWN
PN JP 2000245;
PN JP 2000246;
PD 12-SEP-2000
PP 27-JAN-2000
PP 27-JAN-2000
PP 27-JAN-1909;
PI NITA SHA,JJ
PC C12N15/09;
EH Key
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Gene composition and method.
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JP 2000145487-A/508
J2-5EP-2000
27-JAN-2000 JP 2000019392
27-JAN-1999 US 09/238 402
27-JAN-1999 US 09/238 402
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Location/Qualifiers
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Pred. No. 1
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Pred. No. 1.1e+05;
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DEFINITION
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AUTHORS
TITLE
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AX323400/c
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FEATURES
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KEYWORDS
SOURCE
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AX057285/c
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                                                                                                                                                                                                                                                                                                                           source
                                                                                                                                                                                  264 CCCCCCCTCTCTCTCTCTCTCTCTCTCTCTCTGCTTTCTGT 309
                                                                                                                                                                     Sequence
AX057285
                                                                                                                                                                                                                                                                                                                                                                     Crouzet, J., Scherman, D., Wils, P., Blanche, P. and Cameron, B. Purification of a triple helix formation with an immobilized oligonuclectide
                                                                                                                                                                                                                                                                                                                                                                                                                 synthetic construct.
synthetic construct
artificial sequences.
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Sequence 35 from Patent WO0192511.
AX323400
AX323400.1 GI:18094162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patent: US 6319672-A 35 20-NOV-2001;
Location/Qualifiers
1, 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 (bases 1 to 50)
Crouzet,J., Scherman,D., Wils,P., Blanche,F. and Cameron,B.
Purification of a triple helix formation with an immobilized
oligonucleotide
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                     synthetic construct.
synthetic construct
artificial sequences.
1 (bases 1 to 50)
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Dorner, F.
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nilarity 76.1%;
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/db_xref="taxon:37630"
/note="synthetic oligonucleotide"
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Pred. No. 3.1e+05;
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Job time : 13185 secs
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Best Local Similarity 73.3%;
Matches 33; Conservative
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Patent: WO 0075339-A 16 14-DEC-2000;
Edwards Lifesciences Corporation (US); Baxter Aktiengesellschaft
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Mitochondrian Saccharomyces Cerevisiae
Elkaryoth: Fungi, Saccharomyces: Saccharomycothes; Saccharomycetes;
Saccharomycetles; Saccharomycetaecae; Saccharomyces.
Saccharomyces: Saccharomycetaecae; Saccharomyces.
de Zamaroczy, N., Paugeron-Fonty, G. and Bernardi, G.
Exclaion sequences in the mitochondrial genome of yeast
Gene 21 (3), 193-202 (1963)
c321/0521
                                                                                                                                                                                                                                                 Additional sequences reported in [1], but sequenced in carlier papers, appear in separate entries. Excision repeat corresponds to bases 11 to 33.
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Yeast (S.cerevisiae) mitochondrial petite mutant excision seq
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/db_xref-"taxon:32630"
/note-"annealed oligonucleotide"
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/db_xref-"taxon:4932"
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Pred. No. 1.1e+06;
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Pred. No. 1.3e+06;
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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/SIDS2/gogdata/genesed/geneseqn-embi/NA1991, DMT:
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Best Local Similarity
The invention relates to the isolation of polymorphic repeat sequences having the sequence (d-dh)n, (dd-dT)n which cam be used as genetic markers. Primers based on these sequences can be used to detect these repeats, sepecially for use in e.g paternity or maternity testing, human genetic analysis such as linkage analysis of genetic disease,
                                                                                                                                                                                                                                                                                                                                                                                                                     Detection of polymorphic genetic markers of the form (dC-dA)n(dG-dT)n - using novel nucleic acid mols. as
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21-APR-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    for parentage testing, and in the genetic mapping of economic trait loci, or genes involved the determinism of economically important traits esp. in cattle, to allow selective breeding.

See also AAQ33501-34437.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              266 CCCCTCTCTCTTTTCTCTCTCTCTCTCTTTGCTTGCTTTGTTTCTGT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               rable
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                                                                                                                                                                                                                                                                                                                   Column 13-14; 186pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BP; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  91US-0754351.
89US-0341562.
94US-0222177.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chromosome;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; 0 C; 16 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0.6%;
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Pred. No. 8e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                            mols, as primers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          o;
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CC configuous bases chosen from one of 632 fragments man,78631 to CC AMA7963), where the segment comprises a polymorphic site or an Cc immediately adjacent base, or the complement of the segment, Also Cc described are; (1) an allele specific oligonuclectide that hybridises to ca segment of the novelty; (2) an isolated nuclecticated acid compliance of the novelty where the polymorphic site within the sequence is cocupied by a base other than the reference base indicated in the Cs specification; and (3) analysing a nucleic acid, comprising obtaining a cc nucleic acid from an individual, and determining a base occupying any one of the polymorphic sites of the novelty. The nucleic acid segments and cc method can be used to analyse an individuals nucleic acid segments and cc the polymorphisms. The method can also be used to test for a Cd disease phenotype and correlate the presence of polymorphism. The presence of polymorphism is the presence of polymorphism. The presence of polymorphic sites are useful cfor, e-g. foresasts, paternity testing, correlation of polymorphisms.
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Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                           The present invention describes a nucleic acid segment of 10-100
                                                                                                                                                                                                                                                                                                                                                         Claim 1;
                                                                                                                                                                                                                                                                                                                                                                                                 Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics,
                                                                                                                                                                                                                                                                                                                                                                                       paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27-JAN-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26-JAN-2000; 2000EP-0250023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAA79230 standard; DNA; 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      commercial animal or plant breeding or pedigree analysis. Clones containing the repeat sequences were isolated by hybridisation of chromosome-specific phage libraries with a synthetic poly(dC-dA), (dG-dT) probe. Over 100 repeat blocks were isolated. The inserts from the clones were amplified by primers ART65798-766047. Those clones where the repeat sequence has been determined are shown in ART65704-797. This repeat sequence is from the marker clone wdf122 which contains the repeat sequence having the formula: TTTACAGTAG(CA)17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     medicine; phenotypic trait;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 44 BP; 20 A; 2 C; 18 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      270 CTCTCTCTTTTCTCTCTCTCTCTCTTGCTTGCTTTCTGTAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     43 CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTACTGTAA 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2000-500198/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  genomic DNA; polymorphism; genome; allele-specific; primer;
hybridisation; polymorphic site; forensic; paternity testin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                    Page 22; 141pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Shah N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99US-0238402
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Warrigton JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0.6%;
                                                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 30.8;
Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             analysis; genetic mapping; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  testing;
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Query Match Best Local

Similarity

96.8%;

Score 30.6; DB 2 Pred. No. 9.1e+02

Length 31;

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                                                      contiguous base observibes a nucleic acid segment of 10-100 contiguous bases obsen from one of 632 fragments (AAN#851 to CA AAN#952), where the segment comprises a polymorphic site or an cum mediately where the segment comprises a polymorphic site or an cum mediately where the segment comprises a polymorphic site or an cum mediately of a segment of the segment of the segment of the novelly; (2) an isolated nucleic acid comprising a segment of the novelly; (3) an isolated nucleic acid comprising a comprise by segment of the novelly; where the polymorphic sites within the sequence is cocupied by a base other than the reference hase indicated in the cocupied by a base other than the reference hase indicated in the cocupied by a base other than the reference hase indicated in the cocupied by a base other than the reference hase indicated in the cocupied by a base other than the reference hase indicated in the cocupied by a base other than the reference hase indicated in the cocupied by a base other than the reference hase indicated in the cocupied by a base other than the reference hase indicated acid sequences for nucleic acid sequences for the prison by morphism. The presence of polymorphic sites are useful dearence of polymorphism. The presence of polymorphic sites are useful coff, e.g. forensics, patternity testing, correlation of polymorphisms.

Comprising the presence of polymorphisms of phenotypic traits.

Comprising the containing polymorphic sites. The base occupying the containing polymorphic sites. The base occupying the presence of polymorphic sites are occupying the presence of polymorphic sites are occupying the containing polymorphic sites. The base occupying the presence of polymorphic sites are occupying the polymorphic sites in the presence occupying the presence of phenotypic traits.
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probe; hybridisation; polymorphic site; forensic; paternity testin
medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AA/78631 to AA/79262 represent sequence tags of human genomic DNA fragments containing onlymorphic sites The base occupying the polymorphic site is indicated using IUPAC-IUB nomenclature.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAA79231 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 31 BP; 5 A; 10 C; 8 G; 7 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 1; Page 22; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-500198/45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human genomic DNA polymorphic site sequence tag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26-JAN-2000; 2000EP-0250023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GAGCCTCTCCGAGACRTTGTTCCAGCGACTG 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shah N, Warrigton JA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9905-0238402
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Pred. No. 9.1e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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A; 7 C;

, 7 G;

7 T; 1 other

Matches

30;

Query Match Best Local Similarity

96.8%;

Score 30.6; DB 21; Pred. No. 9.1e+02; 1; Mismatches 0;

Length

31;

0

Gaps

0

Sequence 31 BP;

13

A; 6 C; 5

G; 6 T; 1 other;

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RESULT 5
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                               The present invention describes a nucleic acid segment of 10-100 contiguous bases chosen from one of 632 fragments (AAA78631 to CAA79262), where the segment comprises a polymorphic site or an immediately adjacent base, or the complement of the segment. Also described are: (1) an alial-specific oligonucleotide that hybridises to a segment of the novelty; (2) an isolated nucleic acid comprising a capture of the novelty; (2) an isolated nucleic acid comprising obtaining a sequence of the novelty where the polymorphic site within the sequence is cocupied by a base other than the reference base indicated in the cocupied by a base other than the reference base indicated in the cocupied by a base other than the reference base indicated in the cocupied by a base other than the reference base indicated in the cocupied by a base other than the reference base indicated in the cocupied by a base other than the reference base indicated anyone of the photaling a pose occupied by a base other than the reference of the polymorphic sites in the novelty. The nucleic acid sequences for the presence of polymorphism. The presence of the phonotype with a cocupied by a positional polymorphism. The presence of polymorphic sites are useful containing a polymorphic sites are occupied by the presence of polymorphisms of the presence of polymorphic sites are useful containing polymorphic sites. The base occupied the the compression of phenotype traits.

Containing polymorphic alters. The base occupied the polymorphic site is indicated using IUPAC-IUB nomenclature.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, parentry resting repetit mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAA79232 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                      contiguous bases obser from one of 522 fragments (MAN7631) to AMA79562, where the segment comprises a polymorphic site or an an accomplishment of the segment. Also called the segment comprises a polymorphic site or an accomplishment of the segment. Also called the segment of the segment. Also called the segment of the segment of the segment. Also called the segment of the novelty where the polymorphic site within the segmence is equence of the novelty where the polymorphic site within the segmence is coccupied by a base other than the reference base inclosed in the expectification; and (3) analysing a nucleate acid, comprising obtaining a nucleate acid comprising obtaining a nucleate acid comprising any one of the polymorphic sites of the novelty. The nucleate acid sequences for nucleate acid comprising any one content of the segment of the novelty. The nucleate acid sequences for the presence of polymorphisms, the method can also be used to test for a disease phenotype and correlate the presence of the phenotype with a particular polymorphism, the presence of polymorphism to test for a correlation polymorphism the presence of polymorphic sites are useful conformed to the computation of polymorphisms of the presence of polymorphic sites are useful conformed to the computation of polymorphisms of the presence of polymorphic traits.

AMA78631 to AMA79621 represent sequence tags of human genomic DNA correlation the indicated using IUPAC-IUB nomenclature.
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                                                                   3464 TCCCAGGACACAGGAGTCAAGGCCCAGTGAC 3494
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human genomic polymozphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA79233 standard; DNA; 31 BP
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                                                                                                                                                                                                                                                                                 Sequence 31 BP; 9 A; 10 C; 8 G; 3 T; 1 other;
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                                                                                                                                      Local Similarity
nes 30; Conser
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                                                                                                                                                                       96.8%;
                                                                                                                                                                       Pred.
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                                                                                                                                                                                                              Score 30.6;
                                                                                                                                           Mismatches
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                                                                                                                                                                                                              DB 21;
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RESULT 8
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AMA78631 to AMA79632 represent sequence tags of human genomic DNA correlates and indicated using UPAC-IUB nomenclature.
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                                                                                                                                 3999 AACACCGAGCTCCCGCATCACGCCAAGCACC 4029
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics,
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  AAA79235 standard; DNA;
                                                                                                                                                                                                                                              Sequence 31 BP;
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                                                                                             AACACCGAGCTCCCGYATCACGGCAAGCACC
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                                                                                                                                                                    l Similarity
30; Conserv
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                                                                                                                                                                                      Score 30.6;
Pred. No. 9
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                                                                                                                                                                                                                                                                                                                                                                     contiguous bases obsen from one of 632 fragments (AMA7631) to AMA7632), where the segment comprises a polymorphic site of amendately adjacent base, or the complement of the segment, also amendately adjacent base, or the complement of the segment, also considered are: (1) an allele-specific oligonuclectide that hybridises to a segment of the novelty where the polymorphic site within the sequence is coccupied by a base other than the reference base indicated in the sequence of the novelty where the polymorphic site within the sequence is coccupied by a base other than the reference base indicated in the specificantion; and (3) analysing a nucleic acid, comprising obtaining a nucleic acid from an individual, and determining a base occupying any one of the polymorphic sites of the novelty. The nucleic acid sequences for the presence of polymorphics and correlate the presence of the particular polymorphism. The method can also be used to test for a disease phenotype and correlate the presence of polymorphism that for a disease phenotype, and correlate the presence of polymorphism that of the presence of polymorphic sites are useful correlation and polymorphic traits.

AMA76331 to AMA79322 represent sequence tags of human genomic DNA CC fragments accutating polymorphic sites. The base occupying the XX polymorphics it is a indicated using IUPAC-IUB nomenclature.
                                                                                                                                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe; hybridisation; polymorphic site; forensic; paternity testin medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
                                                                                                                                                                                                       Claim 1; Page 22; 141pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-AUG-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Patil N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26-JAN-2000; 2000EP-0250023
                Human genemic DNA polymorphic site sequence tag SEQ ID NO:606
                                                 20-NOV-2000
                                                                                    AAA79236;
                                                                                                                     AAA79236 standard;
                                                                                                                                                                                                                                                                                                                                             Sequence 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-NOV-2000 (first entry)
                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2000-500198/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           genomic DNA polymorphic site sequence tag SEQ
                                                                                                                                                                                                                                                                            30;
                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Shah N,
                                                                                                                                                                                                                                                                                                                                             BP;
                                                 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0238402
                                                                                                                                                                                                                                                                                                                                           7 A;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Warrigton
                                                                                                                     DNA;
                                                                                                                                                                                                                                                                                          96.8%;
                                                                                                                                                                                                                                                                                                                                             10 C; 8 G; 5 T; 1 other;
                                                                                                                     31 BP
                                                                                                                                                                                                                                                                                          Score 30.6;
Pred. No. 9
                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                    . 9.1e+02;
0;
                                                                                                                                                                                                                                                                                                        Length 31;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1D NO:605
                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          testing;
                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                         0
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Human; gen
probe; hyb
medicine;
Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics, paternity testing, genetic mapping,
                                                                                                              WPI;
                                                                                                                                                                                                                                                                                                                                                                             02-AUG-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                            EP1024200-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
                                                                                                                                                                                                              (AFFY-) AFFYMETRIX INC
                                                                                                                                                                                                                                                                      27-JAN-1999;
                                                                                                                                                                                                                                                                                                                        26-JAN-2000; 2000EP-0250023
                                                                                                              2000-500198/45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            genomic DNA; polymorphism; genome; allele-specific; primer;
hypridisation; polymorphic site; forensic; paternity testin
ne; phenotypic trait; genetic analysis; genetic mapping; ds.
                                                                                                                                                            Shah N,
                                                                                                                                                                                                                                                                      9905-0238402
                                                                                                                                                               Warrigton
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The present invention describes a nucleic acid segment of 10-100 contiguous bases chosen from one of 632 fregments (AMA78631 to CC AMA7963), where the segment comprises a polymorphic site or an CI mediately adjacent base, or the complement of the segment. Also consider the first particular of the segment of the segment of the segment of the novelty here the polymorphic site within the sequence is coccupied by a base other than the reference base indicated in the specification; and (3) analysing a nucleic acid, comprising on the specification; and (3) analysing a nucleic acid, comprising one coupled by a base other than the reference base indicated in the specification; and (3) analysing a nucleic acid, comprising one of the polymorphic sites of the novelty. The nucleic acid sequences for concleic acid from an individual, and determining a base occupying any one of the polymorphic sites an individual a nucleic acid sequences for the presence of polymorphisms. The method can also be used to test for a disease phenotype and correlate the presence of polymorphism to test for a containing polymorphism, the presence of polymorphic sites are useful corresponds properly to traits. AMA78631 to AMA79631 represent sequence tags of human genomic DNA CC fragments containing polymorphic sites. The base occupying the CX CX bases occupying the containing the contai

Claim 1; Page 22; 141pp; English.

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Sequence 31 BP; 2 A;
9 C; 9 G; 10 T; 1 other;
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XAXEXEXEXEXXXX
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                                                                                                                                                           Matches
                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                           4310 TCTGGGTCCCCAGCTCGCTCTTGGTACTTGG 4340
                                                                         AAA79237;
                                                                                        AAA79237 standard; DNA;
                                                                                                                            1 TCTGGGTCCCCAGCTYGCTCTTGGTACTTGG 31
                                                                                                                                                                 Similarity 96.8%;
                                                                                                                                                           Conservative
                                                                                         2
                                                                                                                                                                 Score 30.6; DB 21; Pred. No. 9.1e+02;
                                                                                                                                                                         Length
                                                                                                                                                                           31;
                                                                                                                                                           0
                                                                                                                                                          Gaps
                                                                                                                                                           0
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Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe; hybriddisation; polymorphic site; forensic; paternity testing; medicine; phenotypic trait; genetic analysis; genetic mapping; ds.

polymorphic site sequence tag

SEQ

Ħ NO:607

Human genomic 20-NOV-2000

(first entry) DNA

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC contiguous bases chosen from one of 632 fragments (NAN7863) to CC ANA7963), where the segment comprises a polymorphic site or an CC immediately adjacent base, or the complement of the segment. Also care it also are: (1) an aliele-specific oligonucleotide that hypridises to CC a segment of the novelty (2) an isolated nucleic acid comprising a sequence of the novelty where the polymorphic site within the sequence is CC occupied by a base other than the reference base indicated in the specification; and (3) analysing a nucleic acid, comprising obtaining a cC nucleic acid from an individual, and determining a base occuping any one CC of the polymorphic sites of the novelty. The nucleic acid segments and CC method can be used to analyse an individuals nucleic acid segments and CC method can be used to analyse an individuals nucleic acid segments for the polymorphic sites of the presence of polymorphics. The method can also be used to test for a particular polymorphism. The presence of polymorphic sites are useful for, e.g. forensies, paternity testing, correlation of polymorphisms that and for genetic mapping of phenotypic traits. AAN78631 to AAN79262 represent sequence tags of human genomic DNA CC fragments containing polymorphic sites. The base occupying the CX aAN78631 to AAN79663 to indicated using IUPAC-IUB nomenclature.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                Human, genomic DNA, polymorphism; genome; allele-specific, primer; probe; hybridisation; polymorphic site; forensic; paternity testing; medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
                      02-AUG-2000
                                                        EP1024200-A2
                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                          4339 GGGACCCCAGTGCCTCGTTGAGGGCGCCATT 4369
                                                                                                                                                                                    Human genomic DNA polymorphic site sequence tag SEQ
                                                                                                                                                                                                                          20-NOV-2000
                                                                                                                                                                                                                                                                                          AAA79238 standard; DNA; 31 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 31 BP; 4 A; 9 C; 11 G; 6 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 1; Page 22; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes a nucleic acid segment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patil N, Shah N, Warrigton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27-JAN-1999;
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                                                                                                                                                                                                                                                                                                                                                                           GGGACCCCAGTGCCTYGTTGAGGGCGCCATT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                               30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99US-0238402
                                                                                                                                                                                                                                                                                                                                                                                                                                                          96.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30.6;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                          .1e+02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                      ID NO:608
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
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                                                                                                                                                                                                                                                                                                                                                                                        AAA79239
                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                               Human; genomic DNA; polymorphism; genome; allele-specific; primer; probe; hybridisation; polymorphic site; forensic; paternity testim medicine; phenotypic trait; genetic analysis; genetic mapping; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4449 GATCGAACACTCATGATGTGCCAAGTGCTGT 4479
(AFFY-) AFFYMETRIX INC
                                 27-JAN-1999;
                                                               26-JAN-2000;
                                                                                                   02-AUG-2000
                                                                                                                                  EP1024200-A2
                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                 Human genomic DNA polymorphic site sequence tag
                                                                                                                                                                                                                                                                                                     20-NOV-2000
                                                                                                                                                                                                                                                                                                                                                                  AAA79239 standard; DNA; 31 BP
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1 GATCGAACACTCATGRTGTGCCAAGTGCTGT 31

(first entry)

SEQ

ij NO:609

testing;

2000EP-0250023

99US-0238402

Conservative

96.8%;

Score 30.6; DB Pred. No. 9.1e+(Mismatches

9.1e+02 21; 0

Indels Length

Gaps

0

31; 0

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The present invention describes a nucleic acid segment of 10-100 cc contiguous bases chosen from one of 632 fragments (AAA78631 to AAA78631) to CAAA78631, where the segment comprises a polymorphic site or an CC immediately adjacent base, or the complement of the segment. Also CC described are: (1) an alleis-specific oligonuclectide that hybridises to a segment of the novelty where the polymorphic site within the sequence is coccupied by a base other than the reference base indicated in the sequence of the novelty where the polymorphic site within the sequence is coccupied by a base other than the reference base indicated in the specification; and (3) analysing a nucleic acid, comprising on the inclusive acid from an individual, and determining a base occupying any one of the polymorphic sites of the novelty. The nucleic acid sequences for the presence of polymorphisms, The method can also be used to test for a disease phenotype and correlate the presence of the phenotype with a particular polymorphism. The presence of polymorphisms the correlation of polymorphisms with phenotypic traits and for genetic mapping of phenotypic traits. AAA78631 to AAA79631 to AAA79631
Sequence 31 BP; 7 A; 7 C; 8 G; 8 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 22; 141pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human genomic polymorphic nucleic acid segments, allele specific primers and probes, and methods of analysis, useful for e.g. forensics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               primers and probes, and methods of a paternity testing, genetic mapping,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (AFFY-) AFFYMETRIX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            26-JAN-2000; 2000EP-0250023
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RESULT 13
AAQ33615/c
ID AAQ336
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Best Local Similarity
Matches 30; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4722 GCTTTAGCTAAAGTCCCGCGGGTTCCGGCAT 4752
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PCR; selection; primers; OPTIPRIM; breeding; cattle; parentage; genetic mapping; traits; amplification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-FEB-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAQ33615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAQ33615 standard; DNA; 48 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention describes a nucleic acid segment of 10-100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 1; Page 22; 141pp; English.
Polymorphic bovine DNA markers - used in genetic identification,
                                                                       WPI; 1992-284684/34.
                                                                                                                                                                                                                                                             15-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                     06-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09213102-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Microsatellite sequence from clone AGLA33.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Patil N,
                                                                                                                            Georges M,
                                                                                                                                                                                               (GENM-) GENMARK.
                                                                                                                                                                                                                                                                                                                           15-JAN-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 GCTTTAGCTAAAGTCYCGCGGGTTCCGGCAT 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shah
                                                                                                                            маѕвеу Эм
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                      92WO-US00340
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 30.6; DB 21
Pred. No. 9.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21,
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AAS21107/c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cc The sequence is that of a bovine microsatellite sequence obd. by ccreening a library of bovine microsatellites of between cc 50 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. Cc 750 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. Cc 750 and 500 by with an (AC)15 and a (TC)15 oligonucleotide probe. Cc 750 by 50 and 500 by 50 and 50 and 500 by 50 and 500 by 50 and 500 by 50 and 500 by 50 and 50 and 500 by 50 and 50 and 500 by 50 and 500 by 50 and 500 by 50 and 500 by 50 and 50 and 500 by 50 and 500 by 50 and 500 by 50 and 500 by 50 and 50 and 500 by 50 and 500 by 50 and 50 and 500 by 50 and 500 
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Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                               Purifying double-stranded (ds) DNA from a solution containing dsDNA and other components, comprises passing the solution through a support comprising a covalently coupled oligonucleotide able to form a triple helix with the dsDNA .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ss; DNA purification; triple helix; plasmid purification
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene mapping, and selective breeding
                                                                                                                                                                                               WPI; 2002-097772/13.
                                                                                                                                                                                                                                                        Crouzet J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001; 2001WO-US17122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             06-DEC-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-MAR-2002
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                                                                                                                                                                                                                                                                                                                  (AVET ) AVENTIS PHARMA SA.
                                                                                                                                                                                                                                                                                                                                                                                26-MAY-2000; 2000US-0580923.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200192511-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_region
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                                                                                                                                                                                                                                                    Scherman D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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1..50
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"GA repeat type"
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Pred. No. 3.8e+03;
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                                                                                                                                                                                                                                                    Blanche F,
                                                                                                                                                                                                                                                    Cameron
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This invention comprises a method of purifying double-stranded DNA from Ca asolution containing the double-stranded DNA mixed with other Camponents, comprising passing the solution through a support comprising Ca a covalently coupled cligonucleotide capable of forming a triple helix with the double-stranded DNA. The method is specific sequence present in the double-stranded DNA. The method is specific sequence components. The new method is a simple, rapid and effective method for DNA purification, and makes it possible to obtain especially high purities with high yields. The method enables DNA to be purified from complex mixtures comprising other nucleic acids, proteins, and the Unicleases and the like. The supports may be readily recycles, and the CMANS obtained display improved properties to pharmaceutical safety. Purther, the method enables only one step contrary to prior art. The present sequence represents a DNA sequence contained within the CP plasmid using the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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        The present sequence is one of a large number of 5' ESTs derived from mRNAs encoding secreted proteins. No ORR has yet been conclusively identified within the present sequence. The 5' ESTs expression total human NRNAs or polyA+ RNAs derived from 30 different tissues. EST sequences usually correspond mainly to the 3' untranslated region (UTR) of the mRNA because they are often obtained from oligo-TH primed cDNA sequences.
                                                                                                                                                                                                                          New nucleic acid that is a 5' expressed sequence tag (5' E7) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTS and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping; ss.
                                                                                                                                                                                Claim 1; SEQ ID 35686; 71pp + CD-ROM; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human secreted protein 5' EST, SEQ ID NO: 35686.
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Local Similarity 76.1%;
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Pred. No. 3.8e+03;
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                                               derived from the 5' ends of mRNAs and even in those cases where longer CDNA sequences have been obtained, the full 5' UPR is rarely included 5' ESTS are derived from mRNAs with intact 5' ends and can therefore be used to obtain full length bonks and genomic DNAs 5' ESTS are also used in disgnostic, forensic, gene therepy and chromosome mapping procedures. They are used to obtain upstream regulatory sequences and to design expression and secretion vectors.
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Query Match
Matches
          Local
        h 0.5%;
Similarity 81.1%;
Conservative
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          Score 28.2; DB 21
Pred. No. 4.3e+03;
Mismatches
                    DB 21;
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Indels Length 50; <u>.</u>. Gaps

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Sequence 50 BP; 21 A; 4 C; 19 G; 3 T; 3 other;

밁 43 CCTCTCTCTCTCTCTCTCCTCCTCCTTCTNGNYCT 7

2003, 21:11:19

269 CCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTT 305

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Search completed: March 11, Job time : 1015 secs

Run on:

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq
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Perfect score:
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                                                                                                                                                Issued_Patents_NA:*

1: /cgn2_6/ptodata/1,

2: /cgn2_6/ptodata/1,

3: /cgn2_6/ptodata/1,

4: /cgn2_6/ptodata/1,

5: /cgn2_6/ptodata/1,

6: /cgn2_6/ptodata/1,
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5273
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                              GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
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/cgn2_6/ptodata/1/lna/5B_COMB.seq;*
/cgn2_6/ptodata/1/lna/6A_COMB.seq;*
/cgn2_6/ptodata/1/lna/6A_COMB.seq;*
/cgn2_6/ptodata/1/lna/6B_COMB.seq;*
/cgn2_6/ptodata/1/lna/backfiles1.seq;*
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                                                                                             US-08-222-177A-385
US-08-933-358-18
US-08-933-358-18
US-08-93-358-20
US-09-541-588-934
US-09-541-588-934
US-09-541-588-934
US-09-541-588-934
US-08-418-122A-15
US-08-418-122A-15
US-08-418-122A-15
US-08-418-122A-15
US-08-418-122A-16
US-08-418-122A-17
US-08-418-123A-17
US-08-418-123A-
Sequence 385, App
Sequence 19, App
Sequence 20, Appl
Sequence 335, App
Sequence 335, App
Sequence 4, Appl
Sequence 28, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 11, Appl
Sequence 12, Appl
Sequence 13, Appl
Sequence 14, Appl
Sequence 14, Appl
Sequence 15, Appl
Sequence 16, Appl
Sequence 17, Appl
Sequence 17, Appl
Sequence 18, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 31, Appl
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                                                                                                                                                                                                                   TRUERIA: (608) 831-2106
TRUERIA: (608) 831-2106
INFORMATION FOR SEQ ID NO: 36
SEQUENCE CHARACTERISTICS:
LENGTH: 44 base pairs
TYPE: nucleic acid
STRANSPENSES: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 385, Application US/0
Patent No. 5582979
GENERAL INFORMATION:
APPLICANT: Weber, James L.
Query Match 0.6%;
Best Local Similarity 83.3%;
Matches 35; Conservative
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                                                                                                                            IMMEDIATE SOURCE:
CLONE: mfd122rs
                                                                                                                                                                              MOLECULE TYPE:
                                                                                                                                                                                                  TOPOLOGY:
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Result

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Indels

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CONFUTEN READABLE FORM:

MEDIUM TIPE: PROPPY disk

MEDIUM TIPE: FLORPY disk

COMPUTEN: IBM PC COMMANIBLE

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PACENITIA Release #1.0, Vection #1.25

CURRENT APPLICATION DATA:

APPLICATION UNMERS: US/08/222,177A

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION HOMER: US 07/341,562

FILING DATE: 21-APR-1949

ATTORNEY/ACENT INFORMATION:

NAME: SAID, Chailes: 09.492

REGISTRATION UNMERS: 30,492

REGISTRATION THE SID.

REGISTRATION TO WINDER: 0965.601

TELEPHONE: (608) 831-2100

TELEPHONE: (608) 831-2100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: LENGTH POLYMORPHISMS IN TITLE OF INVENTION: (dG-dA)n.(dG-dT)n SEQUENCES AND METHODS OF USING NUMBER OF SEQUENCES: 460
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADDRESSE: DeMitt Ross & Stevens, S.C.
STREET: 8000 Excelsior Drive, Suite 401
CIT: Madison
STATE: Wisconsin
CONNTRY: USA
ZIP: 53717-1914
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US-09-235-614-9
US-09-235-614-11
US-09-
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US-08-004-800-16
US-08-413-813-16
Score 30.8;
Pred. No. 65;
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sequence 9, Appl
sequence 9, Appl
sequence 11, Appl
sequence 11, Appl
sequence 1, Appl
sequence 1, Appl
sequence 3, Appl
sequence 4, Appl
sequence 7, Appl
sequence 7, Appl
sequence 16, Appl
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                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence:PRIMER SEQUENCE US-08-933-358-18
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SEQ ID NO 35
LENGTH: 50
                                                                                                                                                             Query Match
Best Local
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                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: PURIFICATION OF A TRIPLE HELLX FORMATION WITH AN TITLE OF INVENTION. HUMBHILZED OLIGONUCLEOTIDE FILE REFERENCE: 03804.0138-01 CURRENT APPLICATION NUMBER: US/09/580,923 CURRENT PILING DATE: 2000-05-26 PRIOR APPLICATION NUMBER: 08/860,038 PRIOR APPLICATION NUMBER: 08/860,038 PRIOR FILMS DATE: 1997-06-09 PRIOR FILMS DATE: 1997-06-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: PCT/FR95/01468 PRIOR FILING DATE: 1995-11-08
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS:
                                                                                                                                           ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: oligonucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
                                                                                                                                 FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: DNA
272 CTCTCTCTTCTCTCTCTCTCTCTCTCTCTGGTTTCTGTAATGAG 315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     270 CTCTCTCTTTCTCTCTCTCTCTTCCTTGCTTCGTTTCTGTAA 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
mes 35; Conserv
                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTAAA
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Blanche, Francis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Crouzet, Joel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wils, Pierre
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                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                         0.5%;
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                                           Score 28; DB 3
Pred. No. 3.6e+
0; Mismatches
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Pred. No. 2.9e+02;
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                                                           3.6e+02
                                             10; Indels
                                                                       Length 47;
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                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/09/641,638
CURRENT FILING DATE: 2000-08-16
PRIOR APPLICATION NUMBER: US 09/502,330
PRIOR FILING DATE: 2000-03-11
PRIOR APPLICATION NUMBER: US 06/133,200
PRIOR FILING DATE: 1999-05-07
PRIOR PPLING DATE: 1999-05-23
PRIOR PPLING DATE: 1999-03-23
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Best Local S
Matches 34
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LENGTH: 48
TYPE: DNA
                                     Query Match
                                                                                                                                                                                                                                   SEQ ID NO 934
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Matches 28;
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                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/119,917
PRIOR FILING DATE: 1999-02-12
NUMBER OF SEQ ID NOS: 1304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE OF INVENTION: BIALIBLIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM FILE REFERENCE: GENEET 051CP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/08/933,358
CURRENT FILING DATE: 1997-09-18
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: DNA BRACKETING LOCUS COMPATIBLE STANDARDS FOR TITLE OF INVENTION: ELECTROPHORESIS FULL REFERENCE: 434001aa
                                                                                                                                                                                                                                                      SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
                                                                                             NAME/KEY: allele
LOCATION: 24
OTHER INFORMATION: 12-836-237 : polymorphic base A or
                                                                                                                                                        FEATURE:
                                                                                                                                                                           ORGANISM: Homo Sapiens
                                                                                                                                                                                              LENGTH: 47
TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     267 CCCCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGTAAT 312
                Local Similarity 80.0%;
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                                                                                                                                                                                                                                                      Patent.pm
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  Conservative
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Pred. No. 7.4e+02;
0; Mismatches 12;
                     Score 25; DB 4;
Pred. No. 2.1e+0;
  Mismatches
                  2.1e+03;
  6;
                                        Length 47;
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Gaps
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271 TCTCTCTTTTCTCTCTCTCTCTTGCTTGGTTT 305

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APPLICANN: CIMMEKOV, 11ya

APPLICANN: COMEN, ANAICE

APPLICANN: COMEN, ANAICE

APPLICANN: COMEN, ANAICE

TITLE OF INVENTION: SHALLELIC MARKERS DERIVED FROM GENOMIC REGIONS CARRYING

TITLE OF INVENTION: GENES INVOLVED IN ARACHIDONIC ACID METABOLISM

FILE REFERENCE: GENEST: 0510-08-16

CURRENT APPLICATION NUMBER: US 09/502,330

PRIOR APPLICATION NUMBER: US 09/502,330

PRIOR APPLICATION NUMBER: US 60/133,200

PRIOR TILING DATE: 2000-02-11

PRIOR APPLICATION NUMBER: US 60/133,200

PRIOR TILING DATE: 1999-03-70

PRIOR APPLICATION NUMBER: US 09/275,267

PRIOR APPLICATION NUMBER: US 60/219,917

PRIOR APPLICATION NUMBER: US 60/219,917

PRIOR APPLICATION NUMBER: US 60/219,917

PRIOR RELING DATE: 1999-03-23

PRIOR RELING DATE: 1999-03-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : FEATURE:
: NAME/KEY: aliele
: LOCATION: 24
: OTHER INFORMATION: 12-836-238 : polymorphic base a or T
US-09-641-658-935
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SOFTWARE: Patent.pm
SEQ ID NO 935
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09281481A Patent No. 6383747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Homo Sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ENGTH:
                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: DAWKINS, ROGET L. and ABBAHAM, Lawrence J.
TITLE OF INVENTION. GENETIC ANALYSIS
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS
                    PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                         STREET: 400 GARDEN
CITY: GARDEN CITY
STATE: NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         271 TCTCTCTTTTCTCTCTCTCTCTCTTGCTTGGTTT 305
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                                                            APPLICATION NUMBER: FILING DATE:
APPLICATION NUMBER:
                                     CLASSIFICATION:
                                                                                                                                                                                                                               COUNTRY: UNITED
ZIP: 11530-0299
                                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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Chumakov, Ilya
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                                                                                                                                                                                                                                                                                                             E: SCULLY SCOTT MURPHY & PRESSER 400 GARDEN CITY PLAZA
                                                                                                                                                                                                                                             UNITED STATES OF AMERICA
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US/08/893,971
                                                                                 US/09/281,481
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Pred. No. 2.1e
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 0.5%;
Best Local Similarity 92.9%;
Matches 26; Conservative
                                                                                                                                                         FILING DATE: 16-JUI-1937

APPLICATION NUMBER: US 232,229

FILING DATE: 29-APR-194

APPLICATION NUMBER: PR3279 (AU)

FILING DATE: 01-APV-1951

PPLICATION NUMBER: PCT/AU92/00583

FILING DATE: 30-CCT-1952

ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PILLING DATE: 16-UL-1997
APPLICATION NUMBER: US 23-229
PILLING DATE: 29-APR-1994
APPLICATION NUMBER: PK2279 (AU)
FILLING DATE: 01-NOV-1991
APPLICATION NUMBER: PCT/AU92/405
FILLING DATE: 30-GCT-199
ATTORNET/AGENT INFORMATION:
NAME: DIGGILIO, PRANKS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: +516 742 4366
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                        TELEFAX: +516 742 4366
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: DAWKINS, ROGET L. and ABRAHAM, Lawrence J.
TITLE OF INVENTION: GENETIC ANALYSIS
NUMBER OF EXPURENCES: 22
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: +516 742 4343
                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION DATA
                                                                              TELEPHONE: +516 742 4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Ploppy disk
COMMUTER: IBM PC compatible
OPERATING SYSTEM: PC -DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                      NAME: DIGIGLIO, FRANK S
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/09/281,481A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: UNITED STATES OF AMERICA
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REFERENCE/DOCKET NUMBER:
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28 base pairs
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Pred. No. 1.
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                                                                                                     RESULT 10
US-08-267-803B-46/c
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US-08-469-802B-28
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APPLICANT: Chung, Mingyi
APPLICANT: Coghbi, Hinda Y.
TITLE OF INTENTION: Gene Sequence for Spinocerebellar Ataxia
PITTE OF THE 
Sequence 46, Application US/08267803B Patent No. 5834183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ouery Match 0.4%; Score 23.6; DB 1; Best Local Similarity 86.7%; Pred No. 4.1e+03; Matches 26; Conservative 0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER ENDABLE FORM:

MEDIUM Type: Flopy disk
COMPUTER: IMM PC COMPALINE
COMPUTER: IMM PC COMPALINE
COMPUTER: IMM PC COMPALINE
COMPUTER: IMM PC COMPALINE
COMPANION SYSTEM: DC-005,VAS-DOS
SOFTWHARE. PRESENTIN PC-005,VAS-DOS
COMPUTERS NAME: UN-095,469,802B
FILING DATE: 06-010,195
FILING DATE: 05-010,195
FILING DATE: 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 32 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                270 CTCTCTCTCTTCTCTCTCTCTCTCT 295
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ZIP: 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0.5%;
Local Similarity 96.2%;
nes 25; Conservative
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TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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o. 5741645
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US-08-267-803B-46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ranum, Laura P.W.

APPLICANT: Chung, Ming Y.I

APPLICANT: Chung, Ming Y.I

APPLICANT: Coynid, Huda Y.

TITLE OF INVENTION: Gene Sequence for Spinocerebellar Ataxia

Patent No. 5834183

TITLE OF INVENTION: Type 1 and Method for Diagnosis

NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:

ADDRESSES: Mucting, Rassch, Gebhardt & Schwappach, P.A.

TREET: P.O. Box 581415
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 15, Application US/08418123A
patent No. 5739208
GENERAL INFORMATION:
APPLICANT: Kandal, Sudhit
TPLICANT: Kandal, Sudhit
TITLE OF INVENTION: Integrated Oligonucleotides
NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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MAME: MCCOTMACK MYTA H.

REGISTRATION NUMBER: 36,602
REFERENCE/POCKET NUMBER: 110.00030120
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-305-1217
TELEPHONE: 612-305-1218
INFORMATION FOR SEQ 1D MO: 46:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: COMPATIBLE
COMPUTER: COMPATIBLE
COMP
                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                          CURRENT APPLICATION DATA:
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LENGTH: 32 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           270 CTCTCTCTCTCTCTCTCTCTCTCTCTCT
                                                                                                     COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 7.0 for Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31 CTCTCTCTCTCTCTCTCTCTGTCATTCT 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box :
CITY: Minneapolis
STATE: MN
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       APPLICATION NUMBER: US/08/418,123A
                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                  60606
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                                                                                                                                                                                                                                                                                                                                                                                                                      U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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DB 2;

Length 32;

0 Gaps

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Query Match
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SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                              TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 14:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: line
MOLECULE TYPE: D
HYPOTHETICAL: NO
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       tent No. 5739308
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REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 93,000-E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
PRICEPAY - 31-72-715-1000
                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 35 base pairs
                                                                                                                                                                                                                             NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 93,000-E
TELECOMHULGATION INVESTATION:
TELEPHONE: 312/715-1000
                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Microsoft Word 7.0 for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,123A
FILMG DATE: APPLI 6, 1895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Kendimalla, Ekambar R.
APPLICANT: Argraval, Sudil
TITUE OF INVENTION: Integrated Oligonucleotides
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS;
                                                    MOLECULE TYPE:
HYPOTHETICAL: N
ANTI-SENSE: YES
                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
                                                                                                                                          TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Chicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 34 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                           STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                         ropology:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Application US/08418123A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             300 South Wacker Drive
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                                                                                                                                                                                                              312/715-1234
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                                                                                                       linea
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DNA (genomic)
                                                                                     DNA (genomic)
                                                                                                                      single
0.4%; Score 23.4; DB 1;
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Length 35;
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US-08-418-123A-12
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Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                Query Match 0.4%;
Best Local Similarity 81.8%;
Matches 27; Conservative
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                                                                                                                                                       Sequence 12, Application US/08418123#
Patent No. 5739308
                                                                                                    GENERAL INFORMATION:
APPLICANT: Kandimalla, Ekambar R.
APPLICANT: Agrawal, Sudhir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTMANE: Microsoft Word 7.0 for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,123A
APPLICATION NUMBER: US/08/418,123A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 93
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: April 6, 1995
CLASSIFICATION: 536
ATTORNEY/ACENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Integrated Oligonucleotides NUMBER OF SEQUENCES: 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kandimalla, Ekambar R. APPLICANT: Agrawal, Sudhir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: D
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                                                                                     TITLE OF INVENTION: Integrated Oligonucleotides
                                                                                                                                                                                                                                                                                             COUNTRY:
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STATE: Illinois
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              ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: 312/715-1000
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Chicago
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SEQUENCE CHARACTERISTICS:
LENGTH: 37 hase pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
TOPOLOGY: linear
HYPOTHETICAL: NO
ANTI-SEMSE: YEE
US-08-418-123A-12
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US-08-418-123A-11
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NAME: Greenfield, Michael S.

REGISTRATION UNBER: 37,142

REFERENCE/POCKET NUMBER: 93,000-E

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

11000RMATION FOR SEQ ID NO: 12:
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COMPUTER REDADABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IN PC compatible
OPERATING SYSTEM: PC-DOS,VMS-DOS
SOSTWARE: MICEOSOIT WORD 7.0 for Windows 95
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/418,123A
FILING DATE: APPLICATION: 536
CLASSIFICATION: 536
CLASSIFICATION: 536
                                                                                                                                                                                                   COMPUTER ERADALE FORM:

MEDIUM TYPE: KIOPY disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: DC-DOS/MS-DOS
SOFTWARE: MICCOSOft Word 7.0 for Windows 95
CURRENT APPLICATION DATA.
PILING DATE: APPLI 6, 1995
CLASSIFICATION: 350 CAL.

POLASSIFICATION: 350 CAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence 11, Application US/08418123A
Patent No. 5739308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 0.4%;
Best Local Similarity 81.8%;
Matches 27; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                TELEFAX: 312/715-1234
INFORMATION FOR SEQ ID NO: 11:
                                                          ATTORNET/AGENT INFORMATION:
NAME: Greenfield, Michael S.
REGISTRATION NUMBER: 37,142
REFERENCE/DOCKET NUMBER: 93,000-E
TELECOMUNICATION INFORMATION:
TELEPHONE: 312/715-1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Tandimilla, Ekambar R.
APPLICANT: Agrawal, Suddir
TYTIE OF INVENTION: Integrated Oligonucleotides
NUMBER OF ENDEMORANS: Integrated Oligonucleotides
CORRESPONDENCY ADDRESS:
CORRESPONDENCY ADDRESS:
ADDRESSE: McCoomell Boehnen Hulbert & Berghoff
OTHERST: JOD South Macker Drive
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263 CCCCCCCCTCTCTCTCTCTCTCTCTCTCTCT 295
                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Chicago
STATE: Illinois
COUNTRY: U.S.A.
ZIP: 60606
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COUNTRY: U.S.A.
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TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO ANTI-SENSE: YES US-08-418-123A-11
                                                                     B
Search completed: March 12, 2003, 02:53:00 Job time: 171 secs
                                                                                                                                Query Match 0.4%;
Best Local Similarity 81.8%;
Matches 27; Conservative
                                                                                                263 CCCCCCCCTCTCTCTCTCTCTCTCTCTCT 295
                                                                                                                                                                                                                                                                               LENGTH: 38 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                2 CGCACCCATCTCTCTCCTCTCTCTCTCTCTCT 34
                                                                                                                                                                                                                                                 DNA (genomic)
                                                                                                                                   0;
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Pred. No. 5e+03;
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Minimum DB
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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seq length: 50
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5273
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://ggn_2_6/picdata/2/pulpna/US06_REM_PUB.seq.*
://ggn_2_6/picdata/2/pulpna/US06_REM_PUB.seq.*
://ggn_2_6/picdata/2/pulpna/US07_REM_PUB.seq.*
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                                                                                  US-09-740-002-5
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US-09-263-959-766
US-09-735-363A-6
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Sequence 16, Appl
Sequence 6, Appli
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Sequence 272, App
Sequence 372, App
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Sequence 4, Appli
Sequence 6, Appli
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Sequence 5,
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Sequence 7,
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Sequence 272
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RESULT 2

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73.3% ative cccaccc	cation US/09782650 009350A1 N: Arnold J. rer, Artur Er, Falko-Guenter Elinger, Fiedrich Gs LifeSciences Co N: Targeted Anglog 05530-000611US ON NUMBER: US/09/7 FE: 2001-02-12 NUMBER: US/09/324 1999-06-01 1999-06-07 1999-06-07 1999-06-07 1999-06-07 NUMBER: PCT/US00/ 12000-05-31 NOS: 24 n Ver: 2.1 n Ver: 2.1 n Ver: 2.1 n Ver: 2.1 cial Sequence	44400000000000000000000000000000000000
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al Similarity 73.3%; Pred. No. 1.6e+03; 33; Conservative 0; Mismatches 12; 1 ACCAGAGACCCGCCACCCGGACGCCGGCGCGCGCGCGCG	h h generation generation 782,650 4,079 7,045 /14988	0 US-09-740-002-10 0 US-09-740-002-9 0 US-09-740-002-9 0 US-09-867-193-8 US-09-867-193-8 US-09-868-195-1279 US-09-868-195-1279 US-09-868-1968-130 US-09-868-1368-13 US-09-988-1368-13 US-09-988-1368-13 US-09-988-1368-13 US-09-988-1368-13 US-09-988-1368-13 US-09-988-1368-13 US-09-988-138-193 US-09-988-138-193 US-09-988-193 US-09-988-193-193 US-09-98-193-193 US-09-98-193 US-09-98-193 US-09-98-193-193 US-09-98-193 US-09-98-193 US-09-98-193 US-09-98-193 US-
Indels 0; Gaps 3942	e e	Sequence 10, Appli Sequence 9, Appli Sequence 8, Appli Sequence 179, Appli Sequence 1195, Appli Sequence 1195, Appli Sequence 110, Appli Sequence 13, Appli Sequence 131, Appli Sequence 131, Appli Sequence 133, Appli Sequence 134, Appli Sequence 144, A
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US-09-263-959-766

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; OTHER INFORMATION: Synthetic Oligonucleotide US-09-735-363A-6
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Patent No. US20020150891A1
                                                                                                        SOFTWARE: PatentIn version 3.0 SEQ ID NO 6 LENGTH: 27
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                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Application US/09735363A Patent No. US20010041681A1
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                                                                                                                                                                                                                                                                              APPLICANT: Filion, Mario
APPLICANT: Filion, Mario
APPLICANT: Filion, Mario
TITLE OF INVENTION: Therapeutically Useful Synthetic Oligonucleotides
TILE REFERENCE: 02811-0191
CURRENT APPLICATION UNBER: US/09/735,363A
CURRENT FILLING DATE: 2000-12-12
CURRENT FILLING DATE: 2000-12-12
                                                                                                                                                                           NUMBER OF SEQ ID NOS: 87
                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/170,325
PRIOR FILING DATE: 1999-12-13
PRIOR APPLICATION UNMBER: 60/228,925
PRIOR FILING DATE: 2000-08-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 37 base pairs
                                           FEATURE:
                                                               ORGANISM: Artificial Sequence
                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 05-MAR-199
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 98104-7092
COMPUTER READABLE FORM:
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APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        REGISTRATION NUMBER: 33,963
REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
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Local Similarity 87.5%;
les 28; Conservation
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STRANDEDNESS: sing
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Seattle
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Pred. No. 1.4e+03;
0; Mismatches 4;
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US-09-740-002-4/c
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                                                                                                                                     GENERAL INFORMATION:
APPLICANT: BRAMS, P
APPLICANT: MORROW,
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Patent No. US20020001798A1
                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
        CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
                                              APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: SEPCIFIC TO RSV F-PROTEIN AND METHODS F
TITLE OF INVENTION: SPECIFIC TO RSV F-PROTEIN AND METHODS F
TITLE OF INVENTION: ANAURACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0273759
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HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES RSV F-PROTEIN AND METHODS FOR THEIR

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US-09-263-959-474/c
                                                                                                                                  US-09-263-959-474
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                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                               4414 ATAATAATAATAATAATAATAAT 4439
                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 920010.426C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
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APPLICANT: Rowen, Lee
APPLICANT: Koop, Ben F.
                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
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28 ATAATAATAATAATAATAATAAT 3
                                                                                 Local Similarity 96.2%;
                                                                                                                                                                                 TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                NAME: McMasters, David D. REGISTRATION NUMBER: 33,963
                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 05-MAR
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                                                                                                                                                                  STRANDEDNESS:
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6300 Columbia Center, 701 Fifth Avenue
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                                                                 Conservative
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                                                                                                                                                    linear
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                                                                                                                                                                  single
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Pred. No. 2
                                                                                 Score 24.4;
Pred. No. 2
                                                                   Mismatches
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                                                                                   .6e+03;
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                                                                                                   Length 28;
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RESULT 6
US-09-263-959-538/c
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                                                                                                                                                                                                                                                                                         US-09-263-959-538
                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNET / AGENT INFORMATION:
ATTORNET / AGENT INFORMATION:
ANAME: MCHASTERS , DAVID D.
REGISTRATION MUMBER: 33,930
REFERENCE/DOCKET MUMBER: 39,930
REJECOMMUNICATION INFORMATION:
TELEPOMEN: (206) 622-4900
TELEPOME: (206) 682-6031
INFORMATION FOR SED ID NO: 538:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
SEQ ID NO 3.
                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 538, Application US/09263959
Patent No. US20020150891A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 98104-7092

COMPUTER READABLE FORM:

MEDIUM TYPE: Ploppy disk

COMPUTER: IBM PC COMPAILTH

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTMARE: PROBENTINE FLORE

SOFTMARE: PROBENT RELEASE #1.0, Version #1.25

CURRENT APPLICATION MOMBER: US/09/263,959

PILITED DATE: 05-0847-1959

PILITED DATE: 05-0847-1959
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                                                                                                                                                                                                                                                                                                 LENGTH: 26 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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APPLICANT: ROOP, BEEF
TITLE OF INVESTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1779
CORRESPONDENCE ANDRESS:
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                                                            26
                                                                                                                                                                                                     Local
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Similarity 96.0%;
24; Conservative
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6300 Columbia Center, 701 Fifth Avenue
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Pred. No. 5
                                                                                                                                                                     Score 23.4; DB 10;
Pred. No. 4.6e+03;
D; Mismatches 1;
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5.1e+03;
hes 7;
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                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: U$/09/740,002
CURRENT FLING DATE: 2000-12-0
PRIOR PELLING DATE: 1909-06-18
PRIOR FILING DATE: 1999-06-18
PRIOR FILING DATE: 1999-06-19
PRIOR FILING DATE: 1999-06-07
PRIOR FILING DATE: 1999
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PATOR FILING DATE: 199-06-18
PATOR APPLICATION NUMBER: 08/48,776
PATOR FILING DATE: 1995-06-07
NUMBER OF SED ID NOS: 27
SOUTHARE: PATOR FILING DATE: 1995-06-07
NUMBER OF SED ID NOS: 27
SOUTHARE: PATORITIN VET. 2.1
SED ID NO 2
LENGTH: 50
TYPE: DNA
ORGANISM: Artificial Sequence
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US-09-740-002-2/c
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US-09-740-002-1/c
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RESULT 9
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Patent No. US20020001798A1
GENERAL INFORMATION: PETER
APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
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Best Local :
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Best Local
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CURRENT APPLICATION NUMBER: U5/09/740,002
CURRENT FILING DATE: 2000-12-20
CURRENT FILING DATE: 2000-12-20
CURRENT FILING DATE: 2000-12-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: BRAMS, PETER
APPLICANT: MORROW, PHILLIP
TITLE OF INVENTION: MEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: SPECIFIC TO RSY F-PROTEIN AND METHODS FOR THEIR
TITLE OF INVENTION: MEUTRATURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
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                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                 Conservative
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2; Mismatche
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Pred. No. 7.2e+03;
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9.3e+03;
ches 7;
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US-09-263-959-862/c
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US-09-988-899-55
                                                                                    SOFTWARE: PatentIn Ver.
SEQ ID NO 55
LENGTH: 44
                                                                                                                                                                                                                                                                                                                   Patent No. US20020102613A1
GENERAL INFORMATION:
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MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/263,959
FILING DATE: 05-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                     PRIOR FILING DATE: 1999-05-18
NUMBER OF SEQ ID NOS: 71
                                                                                                                                                                          PRIOR APPLICATION NUMBER: 99201558.6
                                                                                                                                                                                            PRIOR APPLICATION NUMBER: PCT/US00/13682 PRIOR FILING DATE: 2000-05-18
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/988,899
CURRENT FILING DATE: 2001-11-19
                                                                                                                                                                                                                                                               APPLICANT: HOOGERBOOM, HENDRICUS R.J.M.
TITLE OF INVENTION: MOVILL FAB FRAGMENT LIBRARIES AND METHOD FOR THEIR USE
FILE REFERENCE: DX/003 CON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                 OTHER INFORMATION: Description of Artificial Sequence: Primer
                                                 ORGANISM: Artificial Sequence
                                                                  TYPE: DNA
                                  FEATURE:
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: KOOP, DEE F.
TITLE OF INVENTION: DIAGNOSTIC AND THERAPEUTIC COMPOSITIONS AND METHODS WHICH UTI
NUMBER OF SEQUENCES: 1279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (206) 622-4900
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REFERENCE/DOCKET NUMBER: 920010.426C2
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Pred. No. 8
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US-09-853-526-272
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Best Local S
Matches 29
                                                                                                                           GENERAL INFORMATION:
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Best Local :
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                                                                                      APPLICANT: Cohen, Daniel APPLICANT: Blumenfeld,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: DNA
ORGANISM: Homo Sapiens
                                                                       PPLICANT:
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LOCATION: 24
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LOCATION: 1..47
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1 Similarity 67.4%;
29; Conservative
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; OTHER INFORMATION: complement potential microsequencing oligo 4-38-53.mls2 US-09-853-526-272
                                                                                                                                                                                                        Sequence 272, Application US/09901484A Patent No. US20020119460A1
APPLICANT: Bouguelers, Lydie
TITLE OF INVENTION: PROState Cancer Gene
FILE REFERENCE: GEN-TILINCADE
CURRENT APPLICATION UNDERR: US/09/901,484A
CURRENT FILING DATE: 2001-07-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR FILING DATE: 1990-06-23
PRIOR APPLICATION NUMBER: 08/996,306
PRIOR FILING DATE: 1997-12-22
PRIOR APPLICATION NUMBER: 60/099,658
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 09/218,207
PRIOR APPLICATION NUMBER: 09/218,207
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CURRENT FILING DATE: 2001-05-11
PRIOR APPLICATION NUMBER: 09/338,907
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: primer_bind
LOCATION: 1.23
LOCATION: 1.23
OPHEN IMPOSMATION: potential microsequencing oligo 4-38-63.misl
NAME/KEY: primer_bind
LOCATION: 25.47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: polymorphic fragment 4-38-63, variant version of SEQ ID195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2524 GTGACCGAGTCCTCTGGAAGTCTTATCCCCTGGTGCACGTGGT 2566
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                                                                                                                                                                                                                                                                                                                                               4 AAGTTATAAGAAATCAGGCGGAGGCTAAACTTTTT 39
                                                                                                                       Chumakov, Ilya
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Pred. No. 1
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1.8e+04;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 13, Application US/09845160 Patent No. US20020058045A1 GENERAL INFORMATION:
                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                         SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 42
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Best Local
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CURRENT FILING DATE: 2001-05-01
PRIOR APPLICATION NUMBER: 4P 2001-131688
PRIOR FILING DATE: 2001-04-27
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SEQ ID NO 272
                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MIZUGUCHI, HIROYUKI
APPLICANT: HAYAKAWA, TAKAO
TITLE OF INVENTION: ADEMOVIRUS VECTOR
FILE REFERENCE: 081356/0163
                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: JP 2000-161577
PRIOR FILING DATE: 2000-05-31
NUMBER OF SEQ ID NOS: 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR FILIMG DATE: 1998-09-09
PRIOR APPLICATION NUMBER: US 09/218,207
PRIOR FILING DATE: 1998-12-22
PRIOR APPLICATION NUMBER: US 09/338,907
PRIOR FILIMG DATE: 1999-06-23
                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Oligonuclectide 7.
                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                 ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                            TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/RET: primer_bind

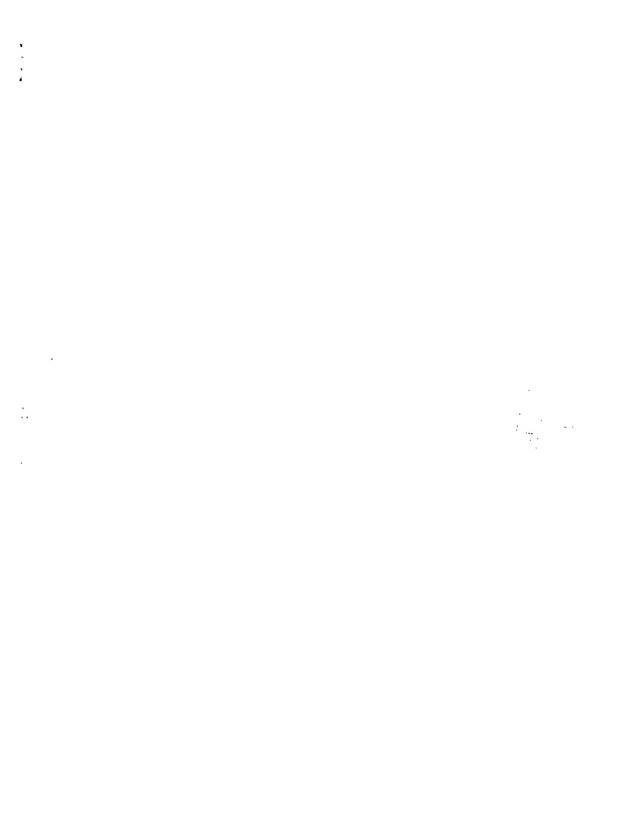
OTHER INFORMATION: potential microsequencing oligo 4-38-63.mls1

NAME/RET: primer_bind

LOCATION: (3)

OTHER INFORMATION: complement potential microsequencing oligo 4-38-63.mls2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR FILING DATE: 2001-05-11
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                                     3922 CGCCGCGGCCGCCGCTGCCAGTCAAGAGCCCGGCGGTGCTGC 3963
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: allele
LOCATION: (24)..(24)
OTHER INFORMATION: polymorphic base G; A in SEQ ID 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LOCATION: (1)..(47)
OTHER INFORMATION: polymorphic fragment 4-38-63, variant version of SEQ ID 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: allele
LOCATION: (1)..(
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                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4 AAGTTATAAGAAAATCAGGCGGAGGCTAAACTTTTT 39
CGCAGCGGCCGCCAGCCGCTCACGCAGCGGCCGTTGCAGC 42
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                                                                                             Score 21.2; DB 1
Pred. No. 2.6e+04
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Pred. No. 2.2e+04;
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Search completed: March 12,
Job time: 321 secs
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                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/193,834
PRIOR FILING DATE: EARLIER FILING DATE: 1998-11-17
NUMBER OF SEQ ID NOS: 44
SOFTMARE: FastSEQ for Windows Version 3.0
SEQ ID NO 44
LENGTH: 50
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 44, Application US/10087523 Publication No. US20020197624A1 GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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Patent No. US20020001798A1
                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Klein, Robert D.
APPLICANT: Brennan, Thomas J.
APPLICANT: Brennan, Thomas J.
TITLE OF INVENTION: SEPTIONS OF CREATING CONSTRUCTS USEFUL FOR INTRODUCING TITLE OF INVENTION: SECURINGS INTO EMBRYONIC STEM CELLS
FILE REFERENCE: 37647000200
CURRENT APPLICATION NUMBER: US/10/087,523
CURRENT FILING DATE: 2007-02-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 08/488,376
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 27
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/740,002
CURRENT FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: 09/335,697
PRIOR FILING DATE: 1999-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: WORROW, PHILLIP
TITLE OF INVENTION: MEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: MEUTRALIZING HIGH AFFINITY HUMAN MONOCLONAL ANTIBODIES
TITLE OF INVENTION: MANUFACTURE AND THERAPEUTIC USE THEREOF
FILE REFERENCE: 037003-0275759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: BRAMS, PETER APPLICANT: MORROW, PHI
                                                                                                                                                                                                                                                                                    TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Description of Artificial Sequence: Primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
                                                                                                            4323 CTCGCTCTTGGTACTTGGGACCCCAGTGCCTCGTTGAGGGCGCCA 4367
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 47
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mes 30; Conserv
                                                                      5 CTCGCTCTGTGCCTTGAACTCCAGTGCCGAGTGTGTGGGGACA 49
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Pred. No.
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Pred. No. 2.8e+04;
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                                                                                                                                                                     3.4e+04;
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Minimum DB seq length: 0 Maximum DB seq length: 50
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AV965544 AV965544
AZ424284 IM0203H14
AZ328467 IM0052E18
AV949200 AV949200
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AUTHORS
TITLE
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KEYWORDS
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COMMENT
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AV674036 Nor1 Satoh uppublished cDNA library Clona intestinalis cDNA clone citb14a20 5', mRNA sequence.
                                                                                                                                        Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-408
Fax: 81-75-705-1113
                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Clonidae; Ciona.

1 (Dases I to 49)
Sauchi,N., Satou,Y., Kohara,Y. and Shin-1,T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
Contact: Nort Satch
Department of Loology
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/organism="Ciona intestinalis"
/db_xref="taxon:7719"
/clone="ofthi420"
/clone_lib="Nor1 Satoh unpublished cDNA library"
                                                                                                      Location/Qualifiers
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8 A2933216
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Mus musculus

Eukaryota; Metezoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalla; Eutheris; Rodentia; Sciurognathi; Muridae; Murinae; Mus

1 (bases 1 to 41)

**Theory M. Herkorin, T., Duval, B., Hamil, C.,
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Department of Zoology
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Satoh.N., Satou.Y., Kohara.Y. and Shin-i.T.
Expressed genes in Ciona intestinalis
Unpublished (2000)
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Tel: 81-75-753-4081
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea; Enterogona; Phlebobranchia; Cionidae; Ciona.
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                                                                                                                                                             house mouse
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ilarity 78.3%;
Conservative
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/dev_stage-"tailbud"
/note-"vector: pabluescript SK"
22 c 5 g 20 t
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/note="Vector: pl
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/clone="type="Nori Satch unpublished cDNA library, egg"
/tissue_type="whole animal"
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/db_xref="taxon:7719"
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                                                                                                                                                                                                                                                    40 bp DNA linear GSS 29-SEP-200
1MO052E18F Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1MO052E18 F, DNA sequence.
A2338467
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University of Utah
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Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmid inserts
                          Eukaryota; Metazoa; Chordatt; Craniata; Veriebrata; Eureleostoni;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
1 (bases 1 to 40)
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Insert Length: 10000 Std Error: 0.00
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    Dunn, D.,
                                                                                                                                  Mus musculus
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Location/Qualifiers
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    Aoyagi, A., Barber, M.,
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/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1N0203N14"
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                                                                 Murinae; Mus.
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RESULT 5
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ORGANISM
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VERSION
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                       REFERENCE
                                                                                                                                                                                                               DEFINITION
                                                                                                                                 KEYWORDS
                                                                                                                                                                                                                                    Locus
     AUTHORS
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                                                                                                                                                                                                                                                                                                                                                          264 CCCCCCCTCTCTCTCTTCTCTCTCTCTCTCTTGCT 299
                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 88.1
nes 32; Conservative
                                                                                                                                                                                                                                                                                                                                      5 CTCTCCCTCTCTCTCTCTCTCTCTCTTTCT 40
                                                                                                                                                                                                             AV949200
AV949200
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University of Utah
University of Utah
Rm. 308, Risman
                                                                                   Ciona intestinalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tel: 801 585 5606
Fax: 801 585 7177
                       Eukaryota; Metazoa; chordata; Urochordata; Ascidlacea; Enterogona; Phlebobtanchla; Ciondae; Ciona.

1 (bases 1 to 47)
                                                                                                                                                   AV949200
AV949200.1 GI:19437499
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Islam, H., Longacre, S., Mahmoud, M., Meenen, E., Pedersen, T., Rellly, M., Rose, M., Rose, R., Stokes, R., Tingey, A., von Niederhausern, A. and Wright, D., Weiss, R.
                                                                                                                                                                                     AV949200 AV949200 AV949200 AV949200 AV949200 AV949200 AV949200 AV94 Satch unpublished cDNA library, larva Cions Intestinalis cDNA clone cliv02g12 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Emall: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error:
Plate: 0052 row: E column: 18
Seq primer: COTTCTAAAACGACGGCCACT
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                plasmid inserts
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10.5 kb range using preparative agarcse gel correction to the variety of pwhole (gl14732114) gb harl29072.1), a copy number inducible derivative of phasmid Ri. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptored mouse DNA was annealed to adaptored vector DNA, and transformed into adaptored vector DNA, and transformed into and selected for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Laboratory Mouse DNN Resource
(http://www.jax.org/resources/documents/dnares/). The DNN
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNN
was blunt end-repaired with 74 DNN polymerase and 74
was blunt end-repaired with 74 DNN polymerase and 78
polymucleotide kinase. Adaptor oligorucleotides were
ligated to the blunt ends in high melar excess. The
adaptored DNN was purified and size-selected for a 9.5 to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /lab_host-*E. Coll strain XIIO-Gold, Tl-resistant, F-*
/note-*Vector: PW462VP, Purified genumic DNA from M.
musculus C57BL/6J_(male) was obtained from the Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Blomedical Polymers Research Bldg., 20 S. 2030 E., SLC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:10090"
/clone="UUGC1M0052E18"
/clone_11b="Mouse 10kb plasmid UUGC1M library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism-"Mus musculus"
/strain-"C57BL/6J"
     Satou, Y., Kohara, Y. and Shin-i, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /sex-"Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                     0.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                 Score 29.6; DB 17;
Pred. No. 1.5e+04;
0; Mismatches 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 40;
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AUTHORS
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KEYWORDS
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Best Local
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Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Orysias latipes
Eukaryota: Methaca; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygli; Neopterygli; Teleostel; Euteleostel; Neoteleostel;
Acanthomorpha; Acanthopterygli; Percomorpha; Athericomorpha;
Eeloniformes; Actianichthyldae; Orysinae; Orysias.

1 (bases 1 to 44)
Kohara; Y., Shin-1, T., Kimura; T., Warita; T., Jindo, T. and Takeda; H.
Medaka EST Project in Takeda's lab
                                                                                                                                                                                                                                                                                                                                                                                          Center For Genetic Resource Information
Mational Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6855
Fax: 81-559-81-6855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BJ001599 MF01SSA CDNA Oryzias latipes CDNA Clone MF01SSA009H08 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kyoto University
Sakyo-ku, Kyoto, Kyoto 606-8502,
Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expressed genes in Clona intestinalis
Unpublished (2000)
Contact: Nori Satch
Department of Coology
                                                                                                                                                                                                                                                                                                                                                    Email: tshini@genes.nig.ac.jp
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Unpublished (2001)
Contact: Tadasu Shin-i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Japanese medaka.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BJ001599.1 GI:17364490
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: satoh@ascidian.zool.kyoto-u.ac.jp.
                                                               Similarity
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Clone clive (Nor! Stoh unpublished cDNA library, larva"
//Lissuc_type who anima!
//dev_tage larva
//dev_tage larva
//note vector: pBluescript SK"
                                                                                                                                       /clone_HMF01SSA009808"
/clone_Hib="MF01SSA chan"
/clone_Hib="MF01SSA chan"
/sex="mixture of female and male"
/tlssuc_type="whole embryo"
/tlssuc_type="whole embryo"
/dev_stage="segmentation stage 20
20 c 5 g 17 t
                                                                                                                                                                                                                                                                   /organism="Oryzias latipes"
/strain="Hd-rR"
/db_xref="taxon:8090"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Ciona intestinalis"
/db_xref="taxon:7719"
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                                                         0.6%;
                                           <u>.</u>.
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Pred. No. 1.8e+04;
                                                         Score 29.2; DB 13; Length Pred, No. 1.9e+04;
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                                           Indels
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                                                                                44;
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                                     Gaps
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0;

268 CCCTCTCTCTTTCTCTCTCTCTCTTGCTTGGTTTCTGT 309

Query Match 0.6%; Score 29.2; DB 17; Length 49; Best Local Similarity 81.0%; Pred. No. 2e-04; Matches 34; Conservative 0; Mismatches 8; Indels

0; Gaps

0

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Query Match
Best Local Similarity
Matches 31; Conserva

Conservative

0.5%;

Score 28.6; DB 17; Pred. No. 2.6e+04; Mismatches

Length 38; Indels

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9 Gaps

0

BASE COUNT ORIGIN

0

/lab host-*s. Coll strain Xil0-Gold, Tiresistant, F-*
//note-*Vector: physical properties of genomic DNA from M.
musculus CSTBL/GU (male) was obtained from the Jackson
Laboratory Mouse DNA Resources/Gocuments/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity The sheared DNA
was blunt end-repaired with Td DNA polymerase and Td
M. Was blunt end-repaired with Td DNA polymerase and Td
M. Polymuclostide kinase. Adaptor oilgound-tectides were
ligated to the blunt ends in high malar excess The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarcse gel
electrophoresis. Vector DNA was prepared from a derivative
of pNA2 (gil473214(gilNa12072.1), a copy-number
inducible derivative of plasmid RI. The vector was lighted
with adaptors complementary to the insert adaptors and
adaptored vector DNA, and transformed into
chemically-competent E. coli XIL0-Gold (Stratagene) cells
and selected for ampicillin resistance.

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ONIGIN SEVER		FEATURES SOUTCE		JOURNAL	TITLE	RESULT 7 AZ846608 LOCUS DEFINITION ACCESSION VERSION V
/Strain* C5/Bi/60; /Strain* C5/Bi/60; /Stone**UGGC2N016F20; /Clone**UGGC2N016F20; /Clone	/organism-"Mus musculus"	12. USA. 1801 S85 5606 1801 S85 7177 1811 dddundgenetics.utah.edu ert Length: 10000 Std Error: 0.00 fc: 0146 row: F column: 20 primer: cACACAGAACACCTYCACC 89: plasmid ends 9: plasmid ends h quality sequence stop: 49. Location/Qualifiers 1. 49	University of Utah Genome Center University of Utah Genome Center University of Utah Rm. 308. Blomedical Polymers Research Bldg. 20 S. 2010 R., SIC. UT		Mouse whole genome scaffolding with paired end reads from 10kb	

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JOURNAL
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KEYWORDS
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AZ479185
LOCUS
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                                                                                                                                source
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0999 row: J Column: 11
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                              University of Utah Genome Center
University of Utah
Rm. 108, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Musinaes I to 38)

Dunn,D., Aoyagi.A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Wahmoud,M., Meenen,E., Pedersen,T., Rellly, M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A., and witcher.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              38 bp DNA linear GSS 04-OCT-200 NA99185 US 04-OCT-200 NA999311R NO299311R NO299311R NDA sequence.
                                                                                                                                                                       High quality sequence stop: 38
                                                                                                                                                                                                                                                                                                    Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                    Unpublished (2000)
Contact: Robert B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid inserts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mouse whole genome scaffolding with paired end reads from 10kb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus
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                                                                                                                                                                                                                                                                                                                                                  34112,
                                                                                                                                                                                                                                                                                                                                                  USA
/db_xref-"taxon:10090"
/clone="UUGC1M0299111"
/clone_lib-"Mouse 10kb plasmid UUGC1M library"
/sex-"Male"
                                                                                  /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                     Location/Qualifiers
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AV947640
                                                                                          JOURNAL COMMENT
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                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutelocstomi; Mammalla; Eutheria; Rodentia; Sciurognathi; Muridae; Musilae; Mamil,C., Daunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,R., Longaere,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Neelss,R.
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Ciona intestinalis.
Ciona intestinalis
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Tel: 81-75-753-4081
Fax: 81-75-705-1113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Nori Satch
Department of Zoology
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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                          Contact: Robert B.
                                                                                                              Unpublished (2000)
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/dev_stage="young adult"
/note="Vector: pBluescript SK"
/note="Vector: 0 g 23 t
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adult"
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/db_xref-"taxon:7719"
/clone-"ciad01g16"
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Eukaryota; Metazoa; C
Mammalia; Eutheria; F
1 (bases 1 to 47)
plasmid inserts
Unpublished (2000)
Contact: Robert B Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Resu
                                                                                                                                                         Dunni,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A. and Wright,D., Neiss,R., Menes,M., Rose,M., Neiss,R., Menes,M., Rose,M., Neiss,R., Menes,M., M., Menes,M., Mene
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Location/Qualifiers
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Insert Length: 10000 Std Error:
Plate: 0062 row: N column: 12
Seg primer: CCTTGTAAAACGACGGCCAGT
Class: plasmid ends
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Fax: 801 585 7177
Emmil: ddunn@gene
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308, Biomedical Polymers Research Bldg.,
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/clone="UUGCIM0062N12"
/clone_1ib="Wouse 10kb plasmid UUGCIM library"
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/organism="Mus musculus"
/strain="C57BL/6J"
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/note="Vector: PWD42nv; Purified genomic DNA from M.
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Pred. No. 2,9e+04;
0; Mismatches 6;
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Location/Qualifiers
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Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
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Tel: 801 585 5606
Fax: 801 585 7177
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Insert Length: 10000 Std Error: 0.00
University of Utah Genome Center University of Utah Rm. 308, Biomedical Polymers Res
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                                                                                               Contact: Robert B.
                                                                                                                          plasmid inserts
Unpublished (2000)
                                                                                                                                                                                          Mouse whole genome scaffolding with paired end reads from 10kb
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musculus C51BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
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/strain="C57BL/6J"
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Pred. No. 3.1e+04;
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Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
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Tel: 801 585 5606
Fax: 801 585 7177
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/clone="UUGC2M0156K04"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
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308, Biomedical Polymers Research Bldg.,

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University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg.,
                                                                                                                                                                                                                            Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C., Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly,M., Rose,M., Rode,R., Stokes,R., Tingey,A., von Niederhausern,A., and Wright,D., Weiss,R.
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1 (Dases 1 to 47)
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Seq primer: CACACAGGAAACAGCTATGACC
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Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                       Contact: Robert B.
                                                                                                                                       Unpublished (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (http://www.jax.org/resources/documents/dnates/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with Ta DNA polymerase and DNA was blunt end-repaired with Ta DNA polymerase and Tax polymerate the blunt ends in high molar access. The ligated to the blunt ends in high molar access. The ligated to the blunt ends in high molar access. The sample repaired the sample of the sample
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/note="Vector: PRD42ny Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
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//lb_xef="taxn:1000"
//clone="UUGC2M0170N09"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BASE COUNT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoka: Metazoa; Chordata; Graniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Primates; Catarrihini; Hominidae; Homo; I (bases I to 49) M. Bowles, L., Dubuque, T., Geisel, G., Jost, S., Krizman, D., Kucaba, T., Lacy, M., Le, N., Lennon, G., Marra, M., Martin, J., Moore, B., Schallenberg, K., Steptoe, M., Tan, F., Theising, B., White, Y., White, T., Waterston, R. and Wilson, R. Washu, N. Lunnon, C. Washu, C. (1997) Contact: Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AN7/3360

49 bp mRNA linear EST 29-JAN-1998 ab55h08.sl Stratagene lung cartinoma 937218 Homo sapiens cDNA clone IMAGE:845727 3' similar to 9:x8557_rnal FOLLICULAR VARIANT TRANSLOCATION PROTEIN 1 PRECURSOR (HUMAN);, mRNA sequence.

AN73350
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: (
Plate: 0174 row: M column: 10
Seq primer: CACACAGGAAACAGCTATGACC
                                                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                High quality sequence stop: 47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Class: plasmid ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 801 585 5606
Fax: 801 585 7177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0.5%;
llarity 76.1%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (http://www.jax.org/resources/documents/dnares/), The DNA was hydrodynamically sheared by repeated phasage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with Ta DNA polymerase and DNA was blunt end-repaired with Ta DNA polymerase and the properties of the blunt ends in high molarate case. The instance the blunt ends in high molarate case are instanced to the blunt ends in high molarate case. The cadeptor of particular was purified and size-malered for a 9.5 to 10.5 be tange using purposes the was prepared from a derivative of ender of the sheared by NP1200721), a copy number induction of the linear taspects and of the sheared adaptored moute DNA was annealed to chemically competent in coli Xill-Gold (Stratagene) cells and spiced for ampicillin resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_11b="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:10090"
/clone="uuGC2M0174M10"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Mus musculus"
/strain="C57BL/6J"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /lab_host-"E. Coli strain XL10-Gold, T1-resistant,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 28.4; DB 17;
Pred. No. 3.1e+04;
0; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7
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Matches

AZ864870 RESULT 14

REFERENCE

JOURNAL TITLE VERSION ACCESSION

KEYWORDS

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Search completed: March 12, 2003, 02:50:06 Job time: 6721 secs
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ORIGIN
                                                                                                           Query Match
Best Local Similarity
Matches 32; Conserv
                                                                                                                                                                                                                                                                                                                                                                                       source
                                                       Fax: 314 286 1810

Email: estewatson.wustl.edu

Email: estewatson.wustl.edu

This clone is available royalty-free through LINL; contact the

This clone is available royalty-free through LINL; contact the

THAGE Consortium (infoélmage.linl.gov) for further information.

Trace considered overall poor quality

Seq primer: -40m.3 fwd. ET from Amersham

High quality sequence stop: 1.

Location/Qualifiers
                                                                                                             0.5%;
milarity 84.2%;
Conservative
                                                                                                                                                                             0
                                                                                                                                                                                                                                                                                                                                                             /organism="Homo sapiens"
/db_xref="taxon:9606"
                                                                                                             Score 28.4; DB 9;
Pred. No. 3.2e+04;
0; Mismatches 6;
                                                                                                                                           Length 49;
                                                                                                                   Indels
                                                                                                                   0
                                                                                                                   Gaps
                                                                                                                     0;
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